

SEQUENCE LISTING

<110> ROEWKAMP, Walter
ROSE-JOHN, Stefan

<120> CONJUGATE FOR MODIFYING INTERACTIONS BETWEEN PROTEINS

<130> 012627-009

<140> 09/142,471

<141> 1998-11-04

<150> PCT/DE97/00458

<151> 1997-03-07

<150> DE 196 08 813.5

<151> 1996-03-07

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<170> PatentIn Ver. 2.0

<210> 1

<211> 1627

<212> DNA

<213> Unknown

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<222> (34)..(90)

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<222> (91)..(1608)

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<221> CDS

<222> (34)..(1608)

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<223> Description of Unknown Organism: A conjugate
comprising two polypeptides with a mutual
affinity.

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Met Leu Ala Val Gly Cys Ala
-15

ctg ctg gct gcc ctg ctg gcc gcg ccg gga gcg gcg ctg gcc cca agg 102
Leu Leu Ala Ala Leu Leu Ala Ala Pro Gly Ala Ala Leu Ala Pro Arg
-10 -5 -1 1

cgc tgc cct gcg cag gag gtg gca aga ggc gtg ctg acc agt ctg cca 150



Sub
E2

Arg	Cys	Pro	Ala	Gln	Glu	Val	Ala	Arg	Gly	Val	Leu	Thr	Ser	Leu	Pro	
5					10					15					20	
gga	gac	agc	gtg	act	ctg	acc	tgc	ccg	ggg	gta	gag	ccg	gaa	gac	aat	198
Gly	Asp	Ser	Val	Thr	Leu	Thr	Cys	Pro	Gly	Val	Glu	Pro	Glu	Asp	Asn	
			25						30					35		
gcc	act	gtt	cac	tgg	gtg	ctc	agg	aag	ccg	gct	gca	ggc	tcc	cac	ccc	246
Ala	Thr	Val	His	Trp	Val	Leu	Arg	Lys	Pro	Ala	Ala	Gly	Ser	His	Pro	
			40					45					50			
agc	aga	tgg	gct	ggc	atg	gga	agg	agg	ctg	ctg	ctg	agg	tcg	gtg	cag	294
Ser	Arg	Trp	Ala	Gly	Met	Gly	Arg	Arg	Leu	Leu	Leu	Arg	Ser	Val	Gln	
		55					60					65				
ctc	cac	gac	tct	gga	aac	tat	tca	tgc	tac	cgg	gcc	ggc	cgc	cca	gct	342
Leu	His	Asp	Ser	Gly	Asn	Tyr	Ser	Cys	Tyr	Arg	Ala	Gly	Arg	Pro	Ala	
	70					75					80					
ggg	act	gtg	cac	ttg	ctg	gtg	gat	gtt	ccc	ccc	gag	gag	ccc	cag	ctc	390
Gly	Thr	Val	His	Leu	Leu	Val	Asp	Val	Pro	Pro	Glu	Glu	Pro	Gln	Leu	
	85				90					95				100		
tcc	tgc	ttc	cgg	aag	agc	ccc	ctc	agc	aat	gtt	gtt	tgt	gag	tgg	ggc	438
Ser	Cys	Phe	Arg	Lys	Ser	Pro	Leu	Ser	Asn	Val	Val	Cys	Glu	Trp	Gly	
				105					110					115		
cct	cgg	agc	acc	cca	tcc	ctg	acg	aca	aag	gct	gtg	ctc	ttg	gtg	agg	486
Pro	Arg	Ser	Thr	Pro	Ser	Leu	Thr	Thr	Lys	Ala	Val	Leu	Leu	Val	Arg	
			120					125					130			
aag	ttt	cag	aac	agt	ccg	gcc	gaa	gac	ttc	cag	gag	ccg	tgc	cag	tat	534
Lys	Phe	Gln	Asn	Ser	Pro	Ala	Glu	Asp	Phe	Gln	Glu	Pro	Cys	Gln	Tyr	
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tcc	cag	gag	tcc	cag	aag	ttc	tcc	tgc	cag	tta	gca	gtc	ccg	gag	gga	582
Ser	Gln	Glu	Ser	Gln	Lys	Phe	Ser	Cys	Gln	Leu	Ala	Val	Pro	Glu	Gly	
	150					155					160					
gac	agc	tct	ttc	tac	ata	gtg	tcc	atg	tgc	gtc	gcc	agt	agt	gtc	ggg	630
Asp	Ser	Ser	Phe	Tyr	Ile	Val	Ser	Met	Cys	Val	Ala	Ser	Ser	Val	Gly	
	165				170					175					180	
agc	aag	ttc	agc	aaa	act	caa	acc	ttt	cag	ggc	tgt	gga	atc	ttg	cag	678
Ser	Lys	Phe	Ser	Lys	Thr	Gln	Thr	Phe	Gln	Gly	Cys	Gly	Ile	Leu	Gln	
				185					190					195		
cct	gat	ccg	cct	gcc	aac	atc	aca	gtc	act	gac	gtg	gcc	aga	aac	ccc	726
Pro	Asp	Pro	Pro	Ala	Asn	Ile	Thr	Val	Thr	Ala	Val	Ala	Arg	Asn	Pro	
			200					205					210			
cgc	tgg	ctc	agt	gtc	acc	tgg	caa	gac	ccc	cac	tcc	tgg	aac	tca	tct	774
Arg	Trp	Leu	Ser	Val	Thr	Trp	Gln	Asp	Pro	His	Ser	Trp	Asn	Ser	Ser	
	215						220					225				

Sub
E2
cont

ttc tac aga cta cgg ttt gag ctc aga tat cgg gct gaa cgg tca aag	822
Phe Tyr Arg Leu Arg Phe Glu Leu Arg Tyr Arg Ala Glu Arg Ser Lys	
230 235 240	
aca ttc aca aca tgg atg gtc aag gac ctc cag cat cac tgt gtc atc	870
Thr Phe Thr Thr Trp Met Val Lys Asp Leu Gln His His Cys Val Ile	
245 250 255 260	
cac gac gcc tgg agc ggc ctg agg cac gtg gtg cag ctt cgt gcc cag	918
His Asp Ala Trp Ser Gly Leu Arg His Val Val Gln Leu Arg Ala Gln	
265 270 275	
gag gag ttc ggg caa ggc gag tgg agc gag tgg agc ccg gag gcc atg	966
Glu Glu Phe Gly Gln Gly Glu Trp Ser Glu Trp Ser Pro Glu Ala Met	
280 285 290	
ggc acg cct tgg aca gaa tcc agg agt cct cca gct cga gga ggt gga	1014
Gly Thr Pro Trp Thr Glu Ser Arg Ser Pro Pro Ala Arg Gly Gly Gly	
295 300 305	
ggt tct gga ggt gga ggt tct gga ggt gga ggt tct gtc gag cca gta	1062
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Val Glu Pro Val	
310 315 320	
ccc cca gga gaa gat tcc aaa gat gta gcc gcc cca cac aga cag cca	1110
Pro Pro Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro	
325 330 335 340	
ctc acc tct tca gaa cga att gac aaa caa att cgg tac atc ctc gac	1158
Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp	
345 350 355	
ggc atc tca gcc ctg aga aag gag aca tgt aac aag agt aac atg tgt	1206
Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys	
360 365 370	
gaa agc agc aaa gag gca ctg gca gaa aac aac ctg aac ctt cca aag	1254
Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys	
375 380 385	
atg gct gaa aaa gat gga tgc ttc caa tct gga ttc aat gag gag act	1302
Met Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr	
390 395 400	
tgc ctg gtg aaa atc atc act ggt ctt ttg gag ttt gag gta tac cta	1350
Cys Leu Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu	
405 410 415 420	
gag tac ctc cag aac aga ttt gag agt agt gag gaa caa gcc aga gct	1398
Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala	
425 430 435	
gtg cag atg agt aca aaa gtc ctg atc cag ttc ctg cag aaa aag gca	1446
Val Gln Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala	
440 445 450	

Sub
E2
Cov

aag aat cta gat gca ata acc acc cct gac cca acc aca aat gcc agc 1494
 Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser
 455 460 465

ctg ctg acg aag ctg cag gca cag aac cag tgg ctg cag gac atg aca 1542
 Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr
 470 475 480

act cat ctc att ctg cgc agc ttt aag gag ttc ctg cag tcc agc ctg 1590
 Thr His Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu
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agg gct ctt cgg caa atg tagcatgggc accgtcgac 1627
 Arg Ala Leu Arg Gln Met
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<210> 2
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 <223> Description of Unknown Organism: A conjugate
 comprising two polypeptides with a mutual
 affinity.

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Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg
 -1 1 5 10

Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
 15 20 25

Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys
 30 35 40 45

Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg
 50 55 60

Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys
 65 70 75

Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val
 80 85 90

Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser
 95 100 105

Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr
 110 115 120 125

*Sub
E2
cont*

Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp
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 Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys
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 Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met
 160 165 170
 Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe
 175 180 185
 Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val
 190 195 200 205
 Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp
 210 215 220
 Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg
 225 230 235
 Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp
 240 245 250
 Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His
 255 260 265
 Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser
 270 275 280 285
 Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser
 290 295 300
 Pro Pro Ala Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 305 310 315
 Gly Gly Ser Val Glu Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val
 320 325 330
 Ala Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys
 335 340 345
 Gln Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr
 350 355 360 365
 Cys Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu
 370 375 380
 Asn Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln
 385 390 395
 Ser Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu
 400 405 410
 Leu Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser

Sub
 E2
 cont

415	420	425
Ser Glu Glu Gln Ala Arg	Ala Val Gln Met	Ser Thr Lys Val Leu Ile
430	435	440 445
Gln Phe Leu Gln Lys Lys	Ala Lys Asn Leu Asp	Ala Ile Thr Thr Pro
450	455	460
Asp Pro Thr Thr Asn Ala	Ser Leu Leu Thr Lys	Leu Gln Ala Gln Asn
465	470	475
Gln Trp Leu Gln Asp Met	Thr Thr His Leu Ile	Leu Arg Ser Phe Lys
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 <223> Description of Unknown Organism: A conjugate
 comprising two polypeptides with a mutual
 affinity.

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 Met Leu Ala Val Gly Cys Ala
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ctg ctg gct gcc ctg ctg gcc gcg ccg gga gcg gcg ctg gcc cca agg 102
 Leu Leu Ala Ala Leu Leu Ala Ala Pro Gly Ala Ala Leu Ala Pro Arg
 -10 -5 -1 1

cgc tgc cct gcg cag gag gtg gca aga gcc gtg ctg acc agt ctg cca 150
 Arg Cys Pro Ala Gln Glu Val Ala Arg Gly Val Leu Thr Ser Leu Pro
 5 10 15 20

gga gac agc gtg act ctg acc tgc ccg ggg gta gag ccg gaa gac aat 198
 Gly Asp Ser Val Thr Leu Thr Cys Pro Gly Val Glu Pro Glu Asp Asn

*Sub
E2
cont*

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Ala	Thr	Val	His	Trp	Val	Leu	Arg	Lys	Pro	Ala	Ala	Gly	Ser	His	Pro					
		40						45					50							
agc	aga	tgg	gct	ggc	atg	gga	agg	agg	ctg	ctg	ctg	agg	tgc	gtg	cag	294				
Ser	Arg	Trp	Ala	Gly	Met	Gly	Arg	Arg	Leu	Leu	Leu	Arg	Ser	Val	Gln					
		55					60					65								
ctc	cac	gac	tct	gga	aac	tat	tca	tgc	tac	cgg	gcc	ggc	cgc	cca	gct	342				
Leu	His	Asp	Ser	Gly	Asn	Tyr	Ser	Cys	Tyr	Arg	Ala	Gly	Arg	Pro	Ala					
	70					75					80									
ggg	act	gtg	cac	tgg	ctg	gtg	gat	gtt	ccc	ccc	gag	gag	ccc	cag	ctc	390				
Gly	Thr	Val	His	Leu	Leu	Val	Asp	Val	Pro	Pro	Glu	Glu	Pro	Gln	Leu					
	85				90				95					100						
tcc	tgc	ttc	cgg	aag	agc	ccc	ctc	agc	aat	gtt	gtt	tgt	gag	tgg	ggc	438				
Ser	Cys	Phe	Arg	Lys	Ser	Pro	Leu	Ser	Asn	Val	Val	Cys	Glu	Trp	Gly					
				105					110					115						
cct	cgg	agc	acc	cca	tcc	ctg	acg	aca	aag	gct	gtg	ctc	ttg	gtg	agg	486				
Pro	Arg	Ser	Thr	Pro	Ser	Leu	Thr	Thr	Lys	Ala	Val	Leu	Leu	Val	Arg					
			120					125					130							
aag	ttt	cag	aac	agt	ccg	gcc	gaa	gac	ttc	cag	gag	ccg	tgc	cag	tat	534				
Lys	Phe	Gln	Asn	Ser	Pro	Ala	Glu	Asp	Phe	Gln	Glu	Pro	Cys	Gln	Tyr					
		135					140					145								
tcc	cag	gag	tcc	cag	aag	ttc	tcc	tgc	cag	tta	gca	gtc	ccg	gag	gga	582				
Ser	Gln	Glu	Ser	Gln	Lys	Phe	Ser	Cys	Gln	Leu	Ala	Val	Pro	Glu	Gly					
	150					155					160									
gac	agc	tct	ttc	tac	ata	gtg	tcc	atg	tgc	gtc	gcc	agt	agt	gtc	ggg	630				
Asp	Ser	Ser	Phe	Tyr	Ile	Val	Ser	Met	Cys	Val	Ala	Ser	Ser	Val	Gly					
	165				170				175					180						
agc	aag	ttc	agc	aaa	act	caa	acc	ttt	cag	ggc	tgt	gga	atc	ttg	cag	678				
Ser	Lys	Phe	Ser	Lys	Thr	Gln	Thr	Phe	Gln	Gly	Cys	Gly	Ile	Leu	Gln					
				185					190				195							
cct	gat	ccg	cct	gcc	aac	atc	aca	gtc	act	gcc	gtg	gcc	aga	aac	ccc	726				
Pro	Asp	Pro	Pro	Ala	Asn	Ile	Thr	Val	Thr	Ala	Val	Ala	Arg	Asn	Pro					
			200					205					210							
cgc	tgg	ctc	agt	gtc	acc	tgg	caa	gac	ccc	cac	tcc	tgg	aac	tca	tct	774				
Arg	Trp	Leu	Ser	Val	Thr	Trp	Gln	Asp	Pro	His	Ser	Trp	Asn	Ser	Ser					
		215					220					225								
ttc	tac	aga	cta	cgg	ttt	gag	ctc	aga	tat	cgg	gct	gaa	cgg	tca	aag	822				
Phe	Tyr	Arg	Leu	Arg	Phe	Glu	Leu	Arg	Tyr	Arg	Ala	Glu	Arg	Ser	Lys					
	230					235					240									
aca	ttc	aca	aca	tgg	atg	gtc	aag	gac	ctc	cag	cat	cac	tgt	gtc	atc	870				

Sub
E2
cont

Thr	Phe	Thr	Thr	Trp	Met	Val	Lys	Asp	Leu	Gln	His	His	Cys	Val	Ile	
245					250					255					260	
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His	Asp	Ala	Trp	Ser	Gly	Leu	Arg	His	Val	Val	Gln	Leu	Arg	Ala	Gln	
				265					270					275		
gag	gag	ttc	ggg	caa	ggc	gag	tgg	agc	gag	tgg	agc	ccg	gag	gcc	atg	966
Glu	Glu	Phe	Gly	Gln	Gly	Glu	Trp	Ser	Glu	Trp	Ser	Pro	Glu	Ala	Met	
			280					285					290			
ggc	acg	cct	tgg	aca	gaa	tcc	agg	agt	cct	cca	gct	cga	gga	ggg	gga	1014
Gly	Thr	Pro	Trp	Thr	Glu	Ser	Arg	Ser	Pro	Pro	Ala	Arg	Gly	Gly	Gly	
		295					300					305				
ggg	tct	gga	ggg	gga	ggg	tct	gtc	gag	cca	gta	ccc	cca	gga	gaa	gat	1062
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Val	Glu	Pro	Val	Pro	Pro	Gly	Glu	Asp	
	310					315					320					
tcc	aaa	gat	gta	gcc	gcc	cca	cac	aga	cag	cca	ctc	acc	tct	tca	gaa	1110
Ser	Lys	Asp	Val	Ala	Ala	Pro	His	Arg	Gln	Pro	Leu	Thr	Ser	Ser	Glu	
325				330					335						340	
cga	att	gac	aaa	caa	att	ggg	tac	atc	ctc	gac	ggc	atc	tca	gcc	ctg	1158
Arg	Ile	Asp	Lys	Gln	Ile	Arg	Tyr	Ile	Leu	Asp	Gly	Ile	Ser	Ala	Leu	
				345					350					355		
aga	aag	gag	aca	tgt	aac	aag	agt	aac	atg	tgt	gaa	agc	agc	aaa	gag	1206
Arg	Lys	Glu	Thr	Cys	Asn	Lys	Ser	Asn	Met	Cys	Glu	Ser	Ser	Lys	Glu	
			360					365					370			
gca	ctg	gca	gaa	aac	aac	ctg	aac	ctt	cca	aag	atg	gct	gaa	aaa	gat	1254
Ala	Leu	Ala	Glu	Asn	Asn	Leu	Asn	Leu	Pro	Lys	Met	Ala	Glu	Lys	Asp	
			375				380					385				
gga	tgc	ttc	caa	tct	gga	ttc	aat	gag	gag	act	tgc	ctg	gtg	aaa	atc	1302
Gly	Cys	Phe	Gln	Ser	Gly	Phe	Asn	Glu	Glu	Thr	Cys	Leu	Val	Lys	Ile	
	390					395					400					
atc	act	ggg	ctt	ttg	gag	ttt	gag	gta	tac	cta	gag	tac	ctc	cag	aac	1350
Ile	Thr	Gly	Leu	Leu	Glu	Phe	Glu	Val	Tyr	Leu	Glu	Tyr	Leu	Gln	Asn	
405				410					415					420		
aga	ttt	gag	agt	agt	gag	gaa	caa	gcc	aga	gct	gtg	cag	atg	agt	aca	1398
Arg	Phe	Glu	Ser	Ser	Glu	Glu	Gln	Ala	Arg	Ala	Val	Gln	Met	Ser	Thr	
				425				430					435			
aaa	gtc	ctg	atc	cag	ttc	ctg	cag	aaa	aag	gca	aag	aat	cta	gat	gca	1446
Lys	Val	Leu	Ile	Gln	Phe	Leu	Gln	Lys	Lys	Ala	Lys	Asn	Leu	Asp	Ala	
			440				445					450				
ata	acc	acc	cct	gac	cca	acc	aca	aat	gcc	agc	ctg	ctg	acg	aag	ctg	1494
Ile	Thr	Thr	Pro	Asp	Pro	Thr	Thr	Asn	Ala	Ser	Leu	Leu	Thr	Lys	Leu	
			455				460					465				

Sub
E2
cont

cag gca cag aac cag tgg ctg cag gac atg aca act cat ctc att ctg 1542
 Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu
 470 475 480

cgc agc ttt aag gag ttc ctg cag tcc agc ctg agg gct ctt cgg caa 1590
 Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln
 485 490 495 500

atg tagcatgggc accgtcgac 1612
 Met

<210> 4
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 <212> PRT
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<223> Description of Unknown Organism: A conjugate
 comprising two polypeptides with a mutual
 affinity.

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Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg
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Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
 15 20 25

Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys
 30 35 40 45

Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg
 50 55 60

Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys
 65 70 75

Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val
 80 85 90

Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser
 95 100 105

Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr
 110 115 120 125

Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp
 130 135 140

Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys

145										150					155															
Gln	Leu	Ala	Val	Pro	Glu	Gly	Asp	Ser	Ser	Phe	Tyr	Ile	Val	Ser	Met															
	160						165						170																	
Cys	Val	Ala	Ser	Ser	Val	Gly	Ser	Lys	Phe	Ser	Lys	Thr	Gln	Thr	Phe															
	175					180						185																		
Gln	Gly	Cys	Gly	Ile	Leu	Gln	Pro	Asp	Pro	Pro	Ala	Asn	Ile	Thr	Val															
	190				195					200					205															
Thr	Ala	Val	Ala	Arg	Asn	Pro	Arg	Trp	Leu	Ser	Val	Thr	Trp	Gln	Asp															
				210					215					220																
Pro	His	Ser	Trp	Asn	Ser	Ser	Phe	Tyr	Arg	Leu	Arg	Phe	Glu	Leu	Arg															
				225				230					235																	
Tyr	Arg	Ala	Glu	Arg	Ser	Lys	Thr	Phe	Thr	Thr	Trp	Met	Val	Lys	Asp															
		240					245					250																		
Leu	Gln	His	His	Cys	Val	Ile	His	Asp	Ala	Trp	Ser	Gly	Leu	Arg	His															
	255					260					265																			
Val	Val	Gln	Leu	Arg	Ala	Gln	Glu	Glu	Phe	Gly	Gln	Gly	Glu	Trp	Ser															
	270				275					280				285																
Glu	Trp	Ser	Pro	Glu	Ala	Met	Gly	Thr	Pro	Trp	Thr	Glu	Ser	Arg	Ser															
				290					295					300																
Pro	Pro	Ala	Arg	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Val	Glu															
			305					310					315																	
Pro	Val	Pro	Pro	Gly	Glu	Asp	Ser	Lys	Asp	Val	Ala	Ala	Pro	His	Arg															
		320				325					330																			
Gln	Pro	Leu	Thr	Ser	Ser	Glu	Arg	Ile	Asp	Lys	Gln	Ile	Arg	Tyr	Ile															
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Leu	Asp	Gly	Ile	Ser	Ala	Leu	Arg	Lys	Glu	Thr	Cys	Asn	Lys	Ser	Asn															
	350				355					360				365																
Met	Cys	Glu	Ser	Ser	Lys	Glu	Ala	Leu	Ala	Glu	Asn	Asn	Leu	Asn	Leu															
				370					375				380																	
Pro	Lys	Met	Ala	Glu	Lys	Asp	Gly	Cys	Phe	Gln	Ser	Gly	Phe	Asn	Glu															
			385					390					395																	
Glu	Thr	Cys	Leu	Val	Lys	Ile	Ile	Thr	Gly	Leu	Leu	Glu	Phe	Glu	Val															
		400					405					410																		
Tyr	Leu	Glu	Tyr	Leu	Gln	Asn	Arg	Phe	Glu	Ser	Ser	Glu	Glu	Gln	Ala															
	415					420					425																			
Arg	Ala	Val	Gln	Met	Ser	Thr	Lys	Val	Leu	Ile	Gln	Phe	Leu	Gln	Lys															
	430				435					440					445															

Sub
E2
cont

Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn
 450 455 460

Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp
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Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser
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Ser Leu Arg Ala Leu Arg Gln Met
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 comprising two polypeptides with a mutual
 affinity.

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Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro Leu Thr
 35 40 45

Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp Gly Ile
 50 55 60

Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser
 65 70 75 80

Ser Pro Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala
 85 90 95

Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu
 100 105 110

Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr
 115 120 125

Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln
 130 135 140

Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn
 145 150 155 160

Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu

*Sub
ES
Cont*

165 170 175
 Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Glu Asp Met Pro Thr His
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Sub
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